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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2008; month=4; day=30; hr=20; min=16; sec=49; ms=897; ]

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\*\*\*\*\*

Reviewer Comments:

SEQUENCE LISTING

<110> Hellström, Mats  
Wallgard, Elisabet  
Kalén, Mattias

Please remove the foreign accent marks in the first and third applicant's names; foreign accent marks are non-ACII characters, which cannot be processed.

<120> ANGIOGENESIS-AFFECTING POLYPEPTIDES, PROTEINS, AND COMPOSITIONS, AND METHODS OF USE THEREOF

The above <120> response exceeds the Sequence Rules' required 72-character line limit: please adjust the line, by inserting hard returns.

(from the end of Sequence 52)

|     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Cys | Ser | Leu | Glu | Pro | Ser | Ala | Pro | Glu | Asp | Leu | Leu |
| 850 |     |     |     |     |     | 855 |     |     |     |     | 860 |     |

Please remove the "1" above, which appears at the end of the submitted file.

\*\*\*\*\*

Application No: 10581761 Version No: 1.0

**Input Set:****Output Set:**

**Started:** 2008-04-15 14:49:57.985  
**Finished:** 2008-04-15 14:50:00.843  
**Elapsed:** 0 hr(s) 0 min(s) 2 sec(s) 858 ms  
**Total Warnings:** 30  
**Total Errors:** 2  
**No. of SeqIDs Defined:** 52  
**Actual SeqID Count:** 52

| Error code | Error Description                                |
|------------|--|
| W 402      | Undefined organism found in <213> in SEQ ID (1)  |
| W 402      | Undefined organism found in <213> in SEQ ID (2)  |
| W 402      | Undefined organism found in <213> in SEQ ID (3)  |
| W 402      | Undefined organism found in <213> in SEQ ID (6)  |
| W 402      | Undefined organism found in <213> in SEQ ID (7)  |
| W 402      | Undefined organism found in <213> in SEQ ID (8)  |
| W 402      | Undefined organism found in <213> in SEQ ID (11) |
| W 402      | Undefined organism found in <213> in SEQ ID (12) |
| W 402      | Undefined organism found in <213> in SEQ ID (13) |
| W 402      | Undefined organism found in <213> in SEQ ID (16) |
| W 402      | Undefined organism found in <213> in SEQ ID (17) |
| W 402      | Undefined organism found in <213> in SEQ ID (18) |
| W 402      | Undefined organism found in <213> in SEQ ID (23) |
| W 402      | Undefined organism found in <213> in SEQ ID (24) |
| W 402      | Undefined organism found in <213> in SEQ ID (25) |
| W 402      | Undefined organism found in <213> in SEQ ID (28) |
| W 402      | Undefined organism found in <213> in SEQ ID (29) |
| W 402      | Undefined organism found in <213> in SEQ ID (30) |
| W 402      | Undefined organism found in <213> in SEQ ID (33) |
| W 402      | Undefined organism found in <213> in SEQ ID (34) |

**Input Set:**

**Output Set:**

**Started:** 2008-04-15 14:49:57.985  
**Finished:** 2008-04-15 14:50:00.843  
**Elapsed:** 0 hr(s) 0 min(s) 2 sec(s) 858 ms  
**Total Warnings:** 30  
**Total Errors:** 2  
**No. of SeqIDs Defined:** 52  
**Actual SeqID Count:** 52

| Error code | Error Description   |
|------------|---|
|            | This error has occurred more than 20 times, will not be displayed |
| E 355      | Empty lines found between the amino acid numbering and the        |
| E 321      | No. of Bases conflict, this line has no nucleotides SEQID (52)    |

<210> 1  
 <211> 736  
 <212> DNA  
 <213> Murinae gen. sp.

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 tccgctcggg ccagacttgc taccatccca ttcgcgggga ccagctggct ctgctggggc 180  
 gcaggactta tcctcgcccg catgagtacc tgtccccagc ggatctcccc aagaattggg 240  
 actggagaaa tgtgaacggg gtcaactatg ccagcgtcac caggaaccag cacatcccac 300  
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 gcaatgctgg ctcttgtaga gggggcaatg accttccggg gtgggagtat gccacaagc 480  
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 taaccagtgt gggacctgca ctgaattcaa agagtgtcac accatccaga attacaccct 600  
 ctggagagtg ggtgattacg gtccctgtcc gggagggaga agatgatggc gagatctatg 660  
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 ggcactctatg ctgagc 736

<210> 2  
 <211> 1404  
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 <213> Murinae gen. sp.

<400> 2  
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 cgggtgcagca gctgcccctg gtgctgctga tgttgctgtt ggcgagtgcg gcacggggcca 180  
 gactctactt ccgctcgggc cagacttgct accatcccat tcgcggggac cagctggctc 240  
 tgctggggcg caggacttat cctcgccgc atgagtacct gtccccagcg gatctcccca 300  
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 acatcccaca gtactgtggg tcctgctggg cccacggcag caccagtgcc atggcagacc 420  
 gaatcaacat caagaggaaa ggtgcatggc cctccatcct gctgtccgta cagaatgtca 480  
 ttgactgtgg caatgctggc tcttgtaga ggggcaatga ccttccggtg tgggagtatg 540

```

cccacaagca tggcatcccc gatgagacct gcaacaacta ccaggccaag gaccaagact    600
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gcacaggtga cagctacaac cttgccatcg agagtgcctg cacatttggg gacccattg   1020
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ctgacactgg acatgtccag acagctataa acagtgcctg tggacatgag gaccagagtg   1140
tggactgcat cccgagagga gacggtaaag gatgaaacac aactgcactg ggaccctccg   1200
ccgtaccctc caggcctgcc tcctccacca ctgagccctc caggcctgcc tcctcttcta   1260
cagtgccttg cttcagccac ccggagaaga gagctatggg ttaggacagc tcaacttata   1320
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tgagtaaaat atctggcttc ccac                                           1404

```

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<210> 3
<211> 306
<212> PRT
<213> Murinae gen. sp.

```

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<400> 3

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Met Ala Ser Ser Gly Ser Val Gln Gln Leu Pro Leu Val Leu Leu Met
1              5              10              15

```

```

Leu Leu Leu Ala Ser Ala Ala Arg Ala Arg Leu Tyr Phe Arg Ser Gly
              20              25              30

```

```

Gln Thr Cys Tyr His Pro Ile Arg Gly Asp Gln Leu Ala Leu Leu Gly
35              40              45

```

```

Arg Arg Thr Tyr Pro Arg Pro His Glu Tyr Leu Ser Pro Ala Asp Leu
50              55              60

```

```

Pro Lys Asn Trp Asp Trp Arg Asn Val Asn Gly Val Asn Tyr Ala Ser
65              70              75              80

```

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Val | Thr | Arg | Asn | Gln | His | Ile | Pro | Gln | Tyr | Cys | Gly | Ser | Cys | Trp | Ala |  |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     | 95  |     |     |     |  |
| His | Gly | Ser | Thr | Ser | Ala | Met | Ala | Asp | Arg | Ile | Asn | Ile | Lys | Arg | Lys |  |
|     |     |     |     | 100 |     |     |     | 105 |     |     |     | 110 |     |     |     |  |
| Gly | Ala | Trp | Pro | Ser | Ile | Leu | Leu | Ser | Val | Gln | Asn | Val | Ile | Asp | Cys |  |
|     |     |     |     | 115 |     |     |     | 120 |     |     |     | 125 |     |     |     |  |
| Gly | Asn | Ala | Gly | Ser | Cys | Glu | Gly | Gly | Asn | Asp | Leu | Pro | Val | Trp | Glu |  |
|     |     |     |     | 130 |     |     |     | 135 |     |     |     | 140 |     |     |     |  |
| Tyr | Ala | His | Lys | His | Gly | Ile | Pro | Asp | Glu | Thr | Cys | Asn | Asn | Tyr | Gln |  |
| 145 |     |     |     | 150 |     |     |     | 155 |     |     |     | 160 |     |     |     |  |
| Ala | Lys | Asp | Gln | Asp | Cys | Asp | Lys | Phe | Asn | Gln | Cys | Gly | Thr | Cys | Thr |  |
|     |     |     |     | 165 |     |     |     | 170 |     |     |     | 175 |     |     |     |  |
| Glu | Phe | Lys | Glu | Cys | His | Thr | Ile | Gln | Asn | Tyr | Thr | Leu | Trp | Arg | Val |  |
|     |     |     |     | 180 |     |     |     | 185 |     |     |     | 190 |     |     |     |  |
| Gly | Asp | Tyr | Gly | Ser | Leu | Ser | Gly | Arg | Glu | Lys | Met | Met | Ala | Glu | Ile |  |
|     |     |     |     | 195 |     |     |     | 200 |     |     |     | 205 |     |     |     |  |
| Tyr | Ala | Asn | Gly | Pro | Ile | Ser | Cys | Gly | Ile | Met | Ala | Thr | Glu | Met | Met |  |
| 210 |     |     |     | 215 |     |     |     | 220 |     |     |     |     |     |     |     |  |
| Ser | Asn | Tyr | Thr | Gly | Gly | Ile | Tyr | Ala | Glu | His | Gln | Asp | Gln | Ala | Val |  |
| 225 |     |     |     | 230 |     |     |     | 235 |     |     |     | 240 |     |     |     |  |
| Ile | Asn | His | Ile | Ile | Ser | Val | Ala | Gly | Trp | Gly | Val | Ser | Asn | Asp | Gly |  |
|     |     |     |     | 245 |     |     |     | 250 |     |     |     | 255 |     |     |     |  |
| Ile | Glu | Tyr | Trp | Ile | Val | Arg | Asn | Ser | Trp | Gly | Glu | Pro | Trp | Gly | Glu |  |
|     |     |     |     | 260 |     |     |     | 265 |     |     |     | 270 |     |     |     |  |
| Lys | Gly | Trp | Met | Arg | Ile | Val | Thr | Ser | Thr | Tyr | Lys | Gly | Gly | Thr | Gly |  |
|     |     |     |     | 275 |     |     |     | 280 |     |     |     | 285 |     |     |     |  |
| Asp | Ser | Tyr | Asn | Leu | Ala | Ile | Glu | Ser | Ala | Cys | Thr | Phe | Gly | Asp | Pro |  |
| 290 |     |     |     | 295 |     |     |     | 300 |     |     |     |     |     |     |     |  |

Ile Val

305

<210> 4

<211> 1480

<212> DNA

<213> Homo sapiens

<400> 4

|   |      |
|---|------|
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| tccgagcggg atccgagcgg ggacccagga gccggcgcgg ggccatggcg aggcgcgggc   | 120  |
| cagggtggcg gccgcttctg ctgctcgtgc tgctggcggg cgcggcgcag ggcggcctct   | 180  |
| acttccgccg gggacagacc tgctaccggc ctctgcgggg ggacgggctg gctccgctgg   | 240  |
| ggcgcagcac atacccccgg cctcatgagt acctgtcccc agcggatctg cccaagagct   | 300  |
| gggactggcg caatgtggat ggtgtcaact atgccagcat cacccggaac cagcacatcc   | 360  |
| cccaatactg cggctcctgc tgggcccacg ccagcaccag cgctatggcg gatcggatca   | 420  |
| acatcaagag gaagggagcg tggccctcca ccctcctgtc cgtgcagaac gtcacgact    | 480  |
| gcggtaacgc tggctcctgt gaagggggta atgacctgtc cgtgtgggac tacgcccacc   | 540  |
| agcacggcat ccctgacgag acctgcaaca actaccaggc caaggaccag gagtgtgaca   | 600  |
| agtttaacca atgtgggaca tgcaatgaat tcaaagagtg ccacgccatc cggaactaca   | 660  |
| ccctctggag ggtgggagac tacggctccc tctctgggag ggagaagatg atggcagaaa   | 720  |
| tctatgcaaa tgggtccatc agctgtggaa taatggcaac agaaagactg gctaactaca   | 780  |
| ccggaggcat ctatgccgaa taccaggaca ccacatatat aaaccatgtc gtttctgtgg   | 840  |
| ctgggtgggg catcagtgat gggactgagt actggattgt ccggaattca tggggtgaac   | 900  |
| catggggcga gagaggctgg ctgaggatcg tgaccagcac ctataaggat gggaagggcg   | 960  |
| ccagatacaa ccttgccatc gaggagcact gtacatttgg ggaccccatc gtttaaggcc   | 1020 |
| atgtcactag aagcgcagtt taagaaaagg catggtgacc catgaccaga ggggatccta   | 1080 |
| tggttatgtg tgccaggctg gctggcagga actgggggtg ctatcaatat tggatggcga   | 1140 |
| ggacagcgtg gcaactggctg cgagtgttcc tgagagttga aagtgggatg acttatgaca  | 1200 |
| cttgcacagc atggctctgc ctcacaaatga tgcagtcagc cacctgggtga agaagtgacc | 1260 |
| tgcgacacag gaaacgatgg gacctcagtc ttcttcagca gaggacttga tattttgtat   | 1320 |
| ttggcaactg tgggcaataa tatggcattt aagaggtgaa agagttcaga cttatcacca   | 1380 |
| ttcttatgtc actttagaat caaggggtggg ggagggaggg agggagttgg cagtttcaaa  | 1440 |



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1480

<210> 5

<211> 303

<212> PRT

<213> Homo sapiens

<400> 5

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1 5 10 15

Leu Ala Gly Ala Ala Gln Gly Gly Leu Tyr Phe Arg Arg Gly Gln Thr  
20 25 30

Cys Tyr Arg Pro Leu Arg Gly Asp Gly Leu Ala Pro Leu Gly Arg Ser  
35 40 45

Thr Tyr Pro Arg Pro His Glu Tyr Leu Ser Pro Ala Asp Leu Pro Lys  
50 55 60

Ser Trp Asp Trp Arg Asn Val Asp Gly Val Asn Tyr Ala Ser Ile Thr  
65 70 75 80

Arg Asn Gln His Ile Pro Gln Tyr Cys Gly Ser Cys Trp Ala His Ala  
85 90 95

Ser Thr Ser Ala Met Ala Asp Arg Ile Asn Ile Lys Arg Lys Gly Ala  
100 105 110

Trp Pro Ser Thr Leu Leu Ser Val Gln Asn Val Ile Asp Cys Gly Asn  
115 120 125

Ala Gly Ser Cys Glu Gly Gly Asn Asp Leu Ser Val Trp Asp Tyr Ala  
130 135 140

His Gln His Gly Ile Pro Asp Glu Thr Cys Asn Asn Tyr Gln Ala Lys  
145 150 155 160

Asp Gln Glu Cys Asp Lys Phe Asn Gln Cys Gly Thr Cys Asn Glu Phe  
165 170 175

Lys Glu Cys His Ala Ile Arg Asn Tyr Thr Leu Trp Arg Val Gly Asp  
180 185 190

Tyr Gly Ser Leu Ser Gly Arg Glu Lys Met Met Ala Glu Ile Tyr Ala  
195 200 205

Asn Gly Pro Ile Ser Cys Gly Ile Met Ala Thr Glu Arg Leu Ala Asn  
210 215 220

Tyr Thr Gly Gly Ile Tyr Ala Glu Tyr Gln Asp Thr Thr Tyr Ile Asn  
225 230 235 240

His Val Val Ser Val Ala Gly Trp Gly Ile Ser Asp Gly Thr Glu Tyr  
245 250 255

Trp Ile Val Arg Asn Ser Trp Gly Glu Pro Trp Gly Glu Arg Gly Trp  
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Leu Arg Ile Val Thr Ser Thr Tyr Lys Asp Gly Lys Gly Ala Arg Tyr  
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Asn Leu Ala Ile Glu Glu His Cys Thr Phe Gly Asp Pro Ile Val  
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<211> 646  
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<213> Murinae gen. sp.

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tttaccaaga ctctttcggg actttcacca tcaatgaatc cagtatagct gattctccaa 180  
gattccctca tagaggaatt ttaattgata catctagaca cttcctgcct gtgaagacaa 240  
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tggacgacca gtctttccct tatcagagta ccacttttcc tgagctaagc aataagggaa 360  
gctactcttt gtctcatgtc tatacaccaa acgatgtccg gatggtgctg gactacgccc 420  
ggctccgagg gattcgagtc ataccagaat ttgatacccc tggccataca cagtcttggg 480  
gcaaaggaca gaaaaacctt ctaactccat gttacaatca aaaaactaaa actcaagtgt 540  
ttgggcctgt agacccaact gtaaacacaa cgtatgcatt cttaacaca tttttcaaag 600

aaatcagcag tgtgtttcca gatcagttca tccacttggg aggaga 646

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<211> 1805

<212> DNA

<213> Murinae gen. sp.

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gctgggtgtcg ctagtgctgc tggccctagt gggcccgccc cgactgcaac ctgcgctatg 180

gcccttcccg cgctcgggtgc agatgttccc gcggctgttg tacatctccg cggaggactt 240

cagcatcgac cacagtccca attccacagc gggcccttcc tgctcgtgc tacaggaggc 300

gtttcggcga tattacaact atgtttttgg tttctacaag agacatcatg gccctgctag 360

atttcgagct gagccacagt tgcagaagct cctgggtctcc attaccctcg agtcagagtg 420

cgagtccttc cctagtctgt ctccagatga aacctattct ctgcttgtag aagaaccagt 480

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gttagtttac caagactctt tcgggacttt caccatcaat gaatccagta tagctgattc 600

tccaagattc cctcatagag gaattttaat tgatacatct agacacttcc tgctgtgaa 660

gacaatttta aaaactctgg atgccatggc ttttaataag tttaatgttc ttcactggca 720

catagtggac gaccagtctt tcccttatca gagtaccact tttcctgagc taagcaataa 780

gggaagctac tctttgtctc atgtctatac accaaaagat gtccggatgg tgctggagta 840

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cttaaagaag aactccattg tttggcaaga agtttttgat gataagggtg agcttcagcc 1260

gggcacagta gtcgaagtgt ggaagagtga gcattattca tatgagctaa agcaagtcac 1320

aggctctggc ttccctgcca tcctttctgc tccttggtac ttagacctga tcagctatgg 1380

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 ccttactcca agattatggc ctcgagcaag cgctgttggg gagagactct ggagccctaa 1560  
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 cagccgtgga atagctgcac aacctctcta tactggatac tgtaactatg agaataaaat 1680  
 atagaagtga cagacgtcta cagcattcca gctatgatca tgttgattct gaaatcatgt 1740  
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<210> 8  
 <211> 536  
 <212> PRT  
 <213> Murinae gen. sp.

<400> 8

Met Pro Gln Ser Pro Arg Ser Ala Pro Gly Leu Leu Leu Leu Gln Ala  
 1 5 10 15

Leu Val Ser Leu Val Ser Leu Ala Leu Val Ala Pro Ala Arg Leu Gln  
 20 25 30

Pro Ala Leu Trp Pro Phe Pro Arg Ser Val Gln Met Phe Pro Arg Leu  
 35 40 45

Leu Tyr Ile Ser Ala Glu Asp Phe Ser Ile Asp His Ser Pro Asn Ser  
 50 55 60

Thr Ala Gly Pro Ser Cys Ser Leu Leu Gln Glu Ala Phe Arg Arg Tyr  
 65 70 75 80

Tyr Asn Tyr Val Phe Gly Phe Tyr Lys Arg His His Gly Pro Ala Arg  
 85 90 95

Phe Arg Ala Glu Pro Gln Leu Gln Lys Leu Leu Val Ser Ile Thr Leu  
 100 105 110

Glu Ser Glu Cys Glu Ser Phe Pro Ser Leu Ser Ser Asp Glu Thr Tyr  
 115 120 125

Ser Leu Leu Val Gln Glu Pro Val Ala Val Leu Lys Ala Asn Ser Val  
 130 135 140

|   |     |     |     |
|---|-----|-----|-----|
| Trp Gly Ala Leu Arg Gly Leu Glu Thr Phe Ser Gln Leu Val Tyr Gln |     |     |     |
| 145   | 150 | 155 | 160 |
|   |     |     |     |
| Asp Ser Phe Gly Thr Phe Thr Ile Asn Glu Ser Ser Ile Ala Asp Ser |     |     |     |
|   | 165 | 170 | 175 |
|   |     |     |     |
| Pro Arg Phe Pro His Arg Gly Ile Leu Ile Asp Thr Ser Arg His Phe |     |     |     |
|   | 180 | 185 | 190 |
|   |     |     |     |
| Leu Pro Val Lys Thr Ile Leu Lys Thr Leu Asp Ala Met Ala Phe Asn |     |     |     |
|   | 195 | 200 | 205 |
|   |     |     |     |
| Lys Phe Asn Val Leu His Trp His Ile Val Asp Asp Gln Ser Phe Pro |     |     |     |
|   | 210 | 215 | 220 |
|   |     |     |     |
| Tyr Gln Ser Thr Thr Phe Pro Glu Leu Ser Asn Lys Gly Ser Tyr Ser |     |     |     |
| 225   | 230 | 235 | 240 |
|   |     |     |     |
| Leu Ser His Val Tyr Thr Pro Asn Asp Val Arg Met Val Leu Glu Tyr |     |     |     |
|   | 245 | 250 | 255 |
|   |     |     |     |
| Ala Arg Leu Arg Gly Ile Arg Val Ile Pro Glu Phe Asp Thr Pro Gly |     |     |     |
|   | 260 | 265 | 270 |
|   |     |     |     |
| His Thr Gln Ser Trp Gly Lys Gly Gln Lys Asn Leu Leu Thr Pro Cys |     |     |     |
|   | 275 | 280 | 285 |
|   |     |     |     |
| Tyr Asn Gln Lys Thr Lys Thr Gln Val Phe Gly Pro Val Asp Pro Thr |     |     |     |
| 290   | 295 | 300 |     |
|   |     |     |     |
| Val Asn Thr Thr Tyr Ala Phe Phe Asn Thr Phe Phe Lys Glu Ile Ser |     |     |     |
| 305   | 310 | 315 | 320 |
|   |     |     |     |
| Ser Val Phe Pro Asp Gln Phe Ile His Leu Gly Gly Asp Glu Val Glu |     |     |     |
|   | 325 | 330 | 335 |
|   |     |     |     |
| Phe Gln Cys Trp Ala Ser Asn Pro Asn Ile Gln Gly Phe Met Lys Arg |     |     |     |
|   | 340 | 345 | 350 |
|   |     |     |     |
| Lys Gly Phe Gly Ser Asp Phe Arg Arg Leu Glu Ser Phe Tyr Ile Lys |     |     |     |
|   | 355 | 360 | 365 |

Lys Ile Leu Glu Ile Ile Ser Ser Leu Lys Lys Asn Ser Ile Val Trp  
370 375 380

Gln Glu Val Phe Asp Asp Lys Val Glu Leu Gln Pro Gly Thr Val Val  
385 390 395 400

Glu Val Trp Lys Ser Glu His Tyr Ser Tyr Glu Leu Lys Gln Val Thr  
405 410 415

Gly Ser Gly Phe Pro Ala Ile Leu Ser Ala Pro Trp Tyr Leu Asp Leu  
420 425 430

Ile Ser Tyr Gly Gln Asp Trp Lys Asn Tyr Tyr Lys Val Glu Pro Leu